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OIPÉ

#3

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/908,992

DATE: 01/31/2002

TIME: 15:55:08

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Output Set: N:\CRF3\01312002\I908992.raw

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3 <110> APPLICANT: SYKEN, JOSH .
4   MUNGER, KARL
6 <120> TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
8 <130> FILE REFERENCE: Hmv-054.01
10 <140> CURRENT APPLICATION NUMBER: 09/908,992
C--> 11 <141> CURRENT FILING DATE: 2002-01-09
13 <150> PRIOR APPLICATION NUMBER: 60/219,718
14 <151> PRIOR FILING DATE: 2000-07-19
16 <150> PRIOR APPLICATION NUMBER: 60/219,537
17 <151> PRIOR FILING DATE: 2000-07-20
19 <160> NUMBER OF SEQ ID NOS: 27
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2656
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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29 <221> NAME/KEY: CDS
30 <222> LOCATION: (32)..(1471)
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35                               1           5
37 cgc tgg ttg ctg gtg gtt gtg ggg acc ccg cgg ctg ccg gct ata tcg      100
38 Arg Trp Leu Leu Val Val Val Gly Thr Pro Arg Leu Pro Ala Ile Ser
39       10           15           20
41 ggt aga ggg gcc cgg ccg ccc agg gag ggc gtg gtg ggg gca tgg ctg      148
42 Gly Arg Gly Ala Arg Pro Pro Arg Glu Gly Val Val Gly Ala Trp Leu
43       25           30           35
45 agc cgc aag ctg agc gtc ccc gcc ttt gcg tct tcc ctg acc tct tgc      196
46 Ser Arg Lys Leu Ser Val Pro Ala Phe Ala Ser Ser Leu Thr Ser Cys
47 40           45           50           55
49 ggc ccc cga gcg ctg ctg aca ttg aga cct ggt gtc agc ctt aca gga      244
50 Gly Pro Arg Ala Leu Leu Thr Leu Arg Pro Gly Val Ser Leu Thr Gly
51       60           65           70
53 aca aaa cat aac cct ttc att tgt act gcc tcc ttc cac acg agt gcc      292
54 Thr Lys His Asn Pro Phe Ile Cys Thr Ala Ser Phe His Thr Ser Ala
55       75           80           85
57 cct ttg gcc aaa gaa gat tat tat cag ata tta gga gtg cct cga aat      340
58 Pro Leu Ala Lys Glu Asp Tyr Tyr Gln Ile Leu Gly Val Pro Arg Asn
59       90           95           100
61 gcc agc cag aaa gag atc aag aaa gcc tat tat cag ctt gcc aag aag      388
62 Ala Ser Gln Lys Glu Ile Lys Lys Ala Tyr Tyr Gln Leu Ala Lys Lys

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63	105	110	115	
65	tat cac cct gac aca aat aag gat gat ccc aaa gcc aag gag aag ttc	436		
66	Tyr His Pro Asp Thr Asn Lys Asp Asp Pro Lys Ala Lys Glu Lys Phe			
67	120	125	130	135
69	tcc cag ctg gca gaa gcc tat gag gtt ttg agt gat gag gtg aag agg	484		
70	Ser Gln Leu Ala Glu Ala Tyr Glu Val Leu Ser Asp Glu Val Lys Arg			
71	140	145	150	
73	aag cag tac gat gcc tac ggc tct gca ggc ttc gat cct ggg gcc agc	532		
74	Lys Gln Tyr Asp Ala Tyr Gly Ser Ala Gly Phe Asp Pro Gly Ala Ser			
75	155	160	165	
77	ggc tcc cag cat agc tac tgg aag gga ggc ccc act gtg gac ccc gag	580		
78	Gly Ser Gln His Ser Tyr Trp Lys Gly Gly Pro Thr Val Asp Pro Glu			
79	170	175	180	
81	gag ctg ttc agg aag atc ttt ggc gag ttc tca tcc tct tca ttt gga	628		
82	Glu Leu Phe Arg Lys Ile Phe Gly Glu Phe Ser Ser Ser Ser Phe Gly			
83	185	190	195	
85	gat ttc cag acc gtg ttt gat cag cct cag gaa tac ttc atg gag ttg	676		
86	Asp Phe Gln Thr Val Phe Asp Gln Pro Gln Glu Tyr Phe Met Glu Leu			
87	200	205	210	215
89	aca ttc aat caa gct gca aag ggg gtc aac aag gag ttc acc gtg aac	724		
90	Thr Phe Asn Gln Ala Lys Gly Val Asn Lys Glu Phe Thr Val Asn			
91	220	225	230	
93	atc atg gac acg tgt gag cgc tgc aac ggc aag ggg aac gag ccc ggc	772		
94	Ile Met Asp Thr Cys Glu Arg Cys Asn Gly Lys Gly Asn Glu Pro Gly			
95	235	240	245	
97	acc aag gtg cag cat tgc cac tac tgt ggc ggc tcc ggc atg gaa acc	820		
98	Thr Lys Val Gln His Cys His Tyr Cys Gly Gly Ser Gly Met Glu Thr			
99	250	255	260	
101	atc aac aca ggc cct ttt gtg atg cgt tcc acg tgt agg aga tgt ggt	868		
102	Ile Asn Thr Gly Pro Phe Val Met Arg Ser Thr Cys Arg Arg Cys Gly			
103	265	270	275	
105	ggc cgc ggc tcc atc atc ata tgc ccc tgt gtg gtc tgc agg gga gca	916		
106	Gly Arg Gly Ser Ile Ile Ile Ser Pro Cys Val Val Cys Arg Gly Ala			
107	280	285	290	295
109	gga caa gcc aag cag aaa aag cga gtg atg atc cct gtg cct gca gga	964		
110	Gly Gln Ala Lys Gln Lys Lys Arg Val Met Ile Pro Val Pro Ala Gly			
111	300	305	310	
113	gtc gag gat ggc cag acc gtg agg atg cct gtg gga aaa agg gaa att	1012		
114	Val Glu Asp Gly Gln Thr Val Arg Met Pro Val Gly Lys Arg Glu Ile			
115	315	320	325	
117	ttc att acg ttc agg gtg cag aaa agc cct gtg ttc cgg agg gac ggc	1060		
118	Phe Ile Thr Phe Arg Val Gln Lys Ser Pro Val Phe Arg Arg Asp Gly			
119	330	335	340	
121	gca gac atc cac tcc gac ctc ttt att tct ata gct cag gct ctt ctt	1108		
122	Ala Asp Ile His Ser Asp Leu Phe Ile Ser Ile Ala Gln Ala Leu Leu			
123	345	350	355	
125	ggg gga aca gcc aga gcc cag ggc ctg tac gag acg atc aac gtg acg	1156		
126	Gly Gly Thr Ala Arg Ala Gln Gly Leu Tyr Glu Thr Ile Asn Val Thr			
127	360	365	370	375

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129 atc ccc cct ggg act cag aca gac cag aag att cgg atg ggt ggg aaa 1204
130 Ile Pro Pro Gly Thr Gln Thr Asp Gln Lys Ile Arg Met Gly Gly Lys
131 380 385 390
133 ggc atc ccc cgg att aac agc tac ggc tac gga gac cac tac atc cac 1252
134 Gly Ile Pro Arg Ile Asn Ser Tyr Gly Tyr Gly Asp His Tyr Ile His
135 395 400 405
137 atc aag ata cga gtt cca aag agg cta acg agc cgg cag cag agc ctg 1300
138 Ile Lys Ile Arg Val Pro Lys Arg Leu Thr Ser Arg Gln Gln Ser Leu
139 410 415 420
141 atc ctg agc tac gcc gag gac gag aca gat gtg gag ggg acg gtg aac 1348
142 Ile Leu Ser Tyr Ala Glu Asp Glu Thr Asp Val Glu Gly Thr Val Asn
143 425 430 435
145 ggc gtc acc ctc acc agc tct ggt ggc agc acc atg gat agc tcc gca 1396
146 Gly Val Thr Leu Thr Ser Ser Gly Gly Ser Thr Met Asp Ser Ser Ala
147 440 445 450 455
149 gga agc aag gct agg cgt gag gct ggg gag gac gag gag gga ttc ctt 1444
150 Gly Ser Lys Ala Arg Arg Glu Ala Gly Glu Asp Glu Glu Gly Phe Leu
151 460 465 470
153 tcc aaa ctt aag aaa atg ttt acc tca tgatatccca gccgaggaaa 1491
154 Ser Lys Leu Lys Lys Met Phe Thr Ser
155 475 480
157 aagatccact ggaaactagg ccgggaagca gcagcccctc caagggccag ggcacctggg 1551
159 agacgggagg attccagaac agcagcactg agctcccacc cgcagagcct ctggacggcc 1611
161 ttggcaacag caaaatcatg ggacaacacc tctctccacg gaaaggtcac agtggacagc 1671
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167 gaatattgtg gatattcttag ttaaaggcca tgcttacagc ttagaaatga agccttaagc 1851
169 tgcatcaagt tacgaagtga ttaatttctt tctcagcaaa cctccgggag gttccagaat 1911
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187 atcattgttt ttctctttgt aaatgttgat tcagaaaagg aaagcacagg ctaagcagtt 2451
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204 <221> NAME/KEY: CDS
205 <222> LOCATION: (1)..(1440)
207 <400> SEQUENCE: 2

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212 ccg cgg ctg ccg gct ata tgc ggt aga ggg gcc cgg ccg ccc agg gag 96
213 Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu
214 20 25 30
216 ggc gtg gtg ggg gca tgg ctg agc cgc aag ctg agc gtc ccc gcc ttt 144
217 Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe
218 35 40 45
220 gcg tct tcc ctg acc tct tgc ggc ccc cga gcg ctg ctg aca ttg aga 192
221 Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
222 50 55 60
224 cct ggt gtc agc ctt aca gga aca aaa cat aac cct ttc att tgt act 240
225 Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
226 65 70 75 80
228 gcc tcc ttc cac acg agt gcc cct ttg gcc aaa gaa gat tat tat cag 288
229 Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
230 85 90 95
232 ata tta gga gtg cct cga aat gcc agc cag aaa gag atc aag aaa gcc 336
233 Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
234 100 105 110
236 tat tat cag ctt gcc aag aag tat cac cct gac aca aat aag gat gat 384
237 Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
238 115 120 125
240 ccc aaa gcc aag gag aag ttc tcc cag ctg gca gaa gcc tat gag gtt 432
241 Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
242 130 135 140
244 ttg agt gat gag gtg aag agg aag cag tac gat gcc tac ggc tct gca 480
245 Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
246 145 150 155 160
248 ggc ttc gat cct ggg gcc agc ggc tcc cag cat agc tac tgg aag gga 528
249 Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly
250 165 170 175
252 ggc ccc act gtg gac ccc gag gag ctg ttc agg aag atc ttt ggc gag 576
253 Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu
254 180 185 190
256 ttc tca tcc tct tca ttt gga gat ttc cag acc gtg ttt gat cag cct 624
257 Phe Ser Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro
258 195 200 205
260 cag gaa tac ttc atg gag ttg aca ttc aat caa gct gca aag ggg gtc 672
261 Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val
262 210 215 220
264 aac aag gag ttc acc gtg aac atc atg gac acg tgt gag cgc tgc aac 720
265 Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn
266 225 230 235 240
268 ggc aag ggg aac gag ccc ggc acc aag gtg cag cat tgc cac tac tgt 768
269 Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys
270 245 250 255
272 ggc ggc tcc ggc atg gaa acc atc aac aca ggc cct ttt gtg atg cgt 816

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277 Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro
278           275           280           285
280 tgt gtg gtc tgc agg gga gca gga caa gcc aag cag aaa aag cga gtg 912
281 Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val
282           290           295           300
284 atg atc cct gtg cct gca gga gtc gag gat ggc cag acc gtg agg atg 960
285 Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met
286 305           310           315           320
288 cct gtg gga aaa agg gaa att ttc att acg ttc agg gtg cag aaa agc 1008
289 Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser
290           325           330           335
292 cct gtg ttc cgg agg gac ggc gca gac atc cac tcc gac ctc ttt att 1056
293 Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile
294           340           345           350
296 tct ata gct cag gct ctt ctt ggg gga aca gcc aga gcc cag ggc ctg 1104
297 Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu
298           355           360           365
300 tac gag acg atc aac gtg acg atc ccc cct ggg act cag aca gac cag 1152
301 Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln
302           370           375           380
304 aag att cgg atg ggt ggg aaa ggc atc ccc cgg att aac agc tac ggc 1200
305 Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly
306 385           390           395           400
308 tac gga gac cac tac atc cac atc aag ata cga gtt cca aag agg cta 1248
309 Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
310           405           410           415
312 acg agc cgg cag cag agc ctg atc ctg agc tac gcc gag gac gag aca 1296
313 Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
314           420           425           430
316 gat gtg gag ggg acg gtg aac ggc gtc acc ctc acc agc tct ggt ggc 1344
317 Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly
318           435           440           445
320 agc acc atg gat agc tcc gca gga agc aag gct agg cgt gag gct ggg 1392
321 Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly
322           450           455           460
324 gag gac gag gag gga ttc ctt tcc aaa ctt aag aaa atg ttt acc tca 1440
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338 <222> LOCATION: (1)..(1359)

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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date